

McKelvey

1636

#5  
8/11/99  
TMC

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/191,647

DATE: 05/11/1999  
TIME: 15:05:48

Input Set: I191647.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

P.S.

ENTERED

1 <110> APPLICANT: Goodman, Corey  
2 Kid, Thomas  
3 Brose, Katja  
4 Tessier-Lavigne, Marc  
5 <120> TITLE OF INVENTION: Modulating Robo: Ligand Interactions  
6 <130> FILE REFERENCE: B98-031-3  
7 <140> CURRENT APPLICATION NUMBER: US/09/191,647  
8 <141> CURRENT FILING DATE: 1998-11-13  
9 <150> EARLIER APPLICATION NUMBER: 60/065,544  
10 <151> EARLIER FILING DATE: 1997-11-14  
11 <150> EARLIER APPLICATION NUMBER: 60/081,057  
12 <151> EARLIER FILING DATE: 1998-04-07  
13 <160> NUMBER OF SEQ ID NOS: 14  
14 <170> SOFTWARE: PatentIn Ver. 2.0  
15 <210> SEQ ID NO 1  
16 <211> LENGTH: 4758  
17 <212> TYPE: DNA  
18 <213> ORGANISM: human  
19 <220> FEATURE:  
20 <221> NAME/KEY: CDS  
21 <222> LOCATION: (1)..(4575)  
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25 1 5 10 15  
26 ctg gcg atc ctg aac aag gtg gca ccg cag gcg tgc ccg gcg cag tgc 96  
27 Leu Ala Ile Leu Asn Lys Val Ala Pro Gln Ala Cys Pro Ala Gln Cys  
28 20 25 30  
29 tct tgc tcg ggc agc aca gtg gac tgt cac ggg ctg gcg ctg cgc agc 144  
30 Ser Cys Ser Gly Ser Thr Val Asp Cys His Gly Leu Ala Leu Arg Ser  
31 35 40 45  
32 gtg ccc agg aat atc ccc cgc aac acc gag aga ctg gat tta aat gga 192  
33 Val Pro Arg Asn Ile Pro Arg Asn Thr Glu Arg Leu Asp Leu Asn Gly  
34 50 55 60  
35 aat aac atc aca aga att acg aag aca gat ttt gct ggt ctt aga cat 240  
36 Asn Asn Ile Thr Arg Ile Thr Lys Thr Asp Phe Ala Gly Leu Arg His  
37 65 70 75 80  
38 cta aga gtt ctt cag ctt atg gag aat aag att agc acc att gaa aga 288  
39 Leu Arg Val Leu Gln Leu Met Glu Asn Lys Ile Ser Thr Ile Glu Arg  
40 85 90 95  
41 gga gca ttc cag gat ctt aaa gaa cta gag aga ctg cgt tta aac aga 336  
42 Gly Ala Phe Gln Asp Leu Lys Glu Leu Glu Arg Leu Arg Leu Asn Arg  
43 100 105 110  
44 aat cac ctt cag ctg ttt cct gag ttg ctg ttt ctt ggg act gcg aag 384

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53	aac	cag	atc	agc	tgt	att	gaa	gat	ggg	gca	ttc	agg	gct	ctc	cgg	gac	528
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56	ctg	gaa	gtg	ctc	act	ctc	aac	aat	aac	aac	att	act	aga	ctt	tct	gtg	576
57	Leu	Glu	Val	Leu	Thr	Leu	Asn	Asn	Asn	Asn	Ile	Thr	Arg	Leu	Ser	Val	
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59	gca	agt	ttc	aac	cat	atg	cct	aaa	ctt	agg	act	ttt	cga	ctg	cat	tca	624
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69	His	Leu	Arg	Gly	His	Asn	Val	Ala	Glu	Val	Gln	Lys	Arg	Glu	Phe	Val	
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71	tgc	agt	gat	gag	gaa	gaa	ggt	cac	cag	tca	ttt	atg	gct	cct	tct	tgt	816
72	Cys	Ser	Asp	Glu	Glu	Glu	Gly	His	Gln	Ser	Phe	Met	Ala	Pro	Ser	Cys	
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74	agt	gtt	ttg	cac	tgc	cct	gcc	gcc	tgt	acc	tgt	agc	aac	aat	atc	gta	864
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76					275								280				285
77	gac	tgt	cgt	ggg	aaa	ggt	ctc	act	gag	atc	ccc	aca	aat	ctt	cca	gag	912
78	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Thr	Glu	Ile	Pro	Thr	Asn	Leu	Pro	Glu	
79					290								295				300
80	acc	atc	aca	gaa	ata	cgt	ttg	gaa	cag	aac	aca	atc	aaa	gtc	atc	cct	960
81	Thr	Ile	Thr	Glu	Ile	Arg	Leu	Glu	Gln	Asn	Thr	Ile	Lys	Val	Ile	Pro	
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83	cct	gga	gct	ttc	tca	cca	tat	aaa	aag	ctt	aga	cga	att	gac	ctg	agc	1008
84	Pro	Gly	Ala	Phe	Ser	Pro	Tyr	Lys	Lys	Leu	Arg	Arg	Ile	Asp	Leu	Ser	
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86	aat	aat	cag	atc	tct	gaa	ctt	gca	cca	gat	gct	ttc	caa	gga	cta	cgc	1056
87	Asn	Asn	Gln	Ile	Ser	Glu	Leu	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Arg	
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89	tct	ctg	aat	tca	ctt	gtc	ctc	tat	gga	aat	aaa	atc	aca	gaa	ctc	ccc	1104
90	Ser	Leu	Asn	Ser	Leu	Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Leu	Pro	
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92	aaa	agt	tta	ttt	gaa	gga	ctg	ttt	tcc	tta	cag	ctc	cta	tta	ttg	aat	1152
93	Lys	Ser	Leu	Phe	Glu	Gly	Leu	Phe	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	
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98	aac ttg aac ctt ctc tcc cta tat gac aac aag ctt cag acc atc gcc	1248
99	Asn Leu Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ala	
100	405 410 415	
101	aag ggg acc ttt tca cct ctt cgg gcc att caa act atg cat ttg gcc	1296
102	Lys Gly Thr Phe Ser Pro Leu Arg Ala Ile Gln Thr Met His Leu Ala	
103	420 425 430	
104	cag aac ccc ttt att tgt gac tgc cat ctc aag tgg cta gcg gat tat	1344
105	Gln Asn Pro Phe Ile Cys Asp Cys His Leu Lys Trp Leu Ala Asp Tyr	
106	435 440 445	
107	ctc cat acc aac ccg att gag acc agt ggt gcc cgt tgc acc agc ccc	1392
108	Leu His Thr Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Thr Ser Pro	
109	450 455 460	
110	cgc cgc ctg gca aac aaa aga att gga cag atc aaa agc aag aaa ttc	1440
111	Arg Arg Leu Ala Asn Lys Arg Ile Gly Gln Ile Lys Ser Lys Lys Phe	
112	465 470 475 480	
113	cgt tgt tca ggt aca gaa gat tat cga tca aaa tta agt gga gac tgc	1488
114	Arg Cys Ser Gly Thr Glu Asp Tyr Arg Ser Lys Leu Ser Gly Asp Cys	
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116	ttt gcg gat ctg gct tgc cct gaa aag tgt cgc tgt gaa gga acc aca	1536
117	Phe Ala Asp Leu Ala Cys Pro Glu Lys Cys Arg Cys Glu Gly Thr Thr	
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119	gta gat tgc tct aat caa aag ctc aac aaa atc ccg gag cac att ccc	1584
120	Val Asp Cys Ser Asn Gln Lys Leu Asn Lys Ile Pro Glu His Ile Pro	
121	515 520 525	
122	cag tac act gca gag ttg cgt ctc aat aat aat gaa ttt acc gtg ttg	1632
123	Gln Tyr Thr Ala Glu Leu Arg Leu Asn Asn Asn Glu Phe Thr Val Leu	
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125	gaa gcc aca gga atc ttt aag aaa ctt cct caa tta cgt aaa ata aac	1680
126	Glu Ala Thr Gly Ile Phe Lys Lys Leu Pro Gln Leu Arg Lys Ile Asn	
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128	ttt agc aac aat aag atc aca gat att gag gag gga gca ttt gaa gga	1728
129	Phe Ser Asn Asn Lys Ile Thr Asp Ile Glu Glu Gly Ala Phe Glu Gly	
130	565 570 575	
131	gca tct ggt gta aat gaa ata ctt ctt acg agt aat cgt ttg gaa aat	1776
132	Ala Ser Gly Val Asn Glu Ile Leu Leu Thr Ser Asn Arg Leu Glu Asn	
133	580 585 590	
134	gtg cag cat aag atg ttc aag gga ttg gaa agc ctc aaa act ttg atg	1824
135	Val Gln His Lys Met Phe Lys Gly Leu Glu Ser Leu Lys Thr Leu Met	
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137	ttg aga agc aat cga ata acc tgt gtg ggg aat gac agt ttc ata gga	1872
138	Leu Arg Ser Asn Arg Ile Thr Cys Val Gly Asn Asp Ser Phe Ile Gly	
139	610 615 620	
140	ctc agt tct gtg cgt ttg ctt tct ttg tat gat aat caa att act aca	1920
141	Leu Ser Ser Val Arg Leu Leu Ser Leu Tyr Asp Asn Gln Ile Thr Thr	
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143	gtt gca cca ggg gca ttt gat act ctc cat tct tta tct act cta aac	1968
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150	Glu	Trp	Leu	Arg	Lys	Lys	Arg	Ile	Val	Thr	Gly	Asn	Pro	Arg	Cys	Gln		
151				675				680						685				
152	aaa	cca	tac	ttc	ctg	aaa	gaa	ata	ccc	atc	cag	gat	gtg	gcc	att	cag		2112
153	Lys	Pro	Tyr	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala	Ile	Gln		
154			690				695						700					
155	gac	ttc	act	tgt	gat	gac	gga	aat	gat	gac	aat	agt	tgc	tcc	cca	ctt		2160
156	Asp	Phe	Thr	Cys	Asp	Asp	Gly	Asn	Asp	Asp	Asn	Ser	Cys	Ser	Pro	Leu		
157			705				710						715			720		
158	tct	cgc	tgt	cct	act	gaa	tgt	act	tgc	ttg	gat	aca	gtc	gtc	cga	tgt		2208
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160				725					730					735				
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165	Thr	Glu	Leu	Tyr	Leu	Asp	Gly	Asn	Gln	Phe	Thr	Leu	Val	Pro	Lys	Glu		
166			755				760						765					
167	ctc	tcc	aac	tac	aaa	cat	tta	aca	ctt	ata	gac	tta	agt	aac	aac	aga		2352
168	Leu	Ser	Asn	Tyr	Lys	His	Leu	Thr	Leu	Ile	Asp	Leu	Ser	Asn	Asn	Arg		
169			770				775						780					
170	ata	agc	acg	ctt	tct	aat	cag	agc	ttc	agc	aac	atg	acc	cag	ctc	ctc		2400
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172			785				790						795			800		
173	acc	tta	att	ctt	agt	tac	aac	cgt	ctg	aga	tgt	att	cct	cct	cgc	acc		2448
174	Thr	Leu	Ile	Leu	Ser	Tyr	Asn	Arg	Leu	Arg	Cys	Ile	Pro	Pro	Arg	Thr		
175				805					810					815				
176	ttt	gat	gga	tta	aag	tct	ctt	cga	tta	ctt	tct	cta	cat	gga	aat	gac		2496
177	Phe	Asp	Gly	Leu	Lys	Ser	Leu	Arg	Leu	Leu	Ser	Leu	His	Gly	Asn	Asp		
178			820					825					830					
179	att	tct	gtt	gtg	cct	gaa	ggt	gct	ttc	aat	gat	ctt	tct	gca	tta	tca		2544
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181			835					840					845					
182	cat	cta	gca	att	gga	gcc	aac	cct	ctt	tac	tgt	gat	tgt	aac	atg	cag		2592
183	His	Leu	Ala	Ile	Gly	Ala	Asn	Pro	Leu	Tyr	Cys	Asp	Cys	Asn	Met	Gln		
184			850				855						860					
185	tgg	tta	tcc	gac	tgg	gtg	aag	tcg	gaa	tat	aag	gag	cct	gga	att	gct		2640
186	Trp	Leu	Ser	Asp	Trp	Val	Lys	Ser	Glu	Tyr	Lys	Glu	Pro	Gly	Ile	Ala		
187			865				870					875				880		
188	cgt	tgt	gct	ggt	cct	gga	gaa	atg	gca	gat	aaa	ctt	tta	ctc	aca	act		2688
189	Arg	Cys	Ala	Gly	Pro	Gly	Glu	Met	Ala	Asp	Lys	Leu	Leu	Leu	Thr	Thr		
190				885					890					895				
191	ccc	tcc	aaa	aaa	ttt	acc	tgt	caa	ggt	cct	gtg	gat	gtc	aat	att	cta		2736
192	Pro	Ser	Lys	Lys	Phe	Thr	Cys	Gln	Gly	Pro	Val	Asp	Val	Asn	Ile	Leu		
193			900						905					910				
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198	Cys Asn Ser Asp Pro Val Asp Phe Tyr Arg Cys Thr Cys Pro Tyr Gly	
199	930 935 940	
200	ttc aag ggg cag gac tgt gat gtc cca att cat gcc tgc atc agt aac	2880
201	Phe Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala Cys Ile Ser Asn	
202	945 950 955 960	
203	cca tgt aaa cat gga gga act tgc cac tta aag gaa gga gaa gaa gat	2928
204	Pro Cys Lys His Gly Gly Thr Cys His Leu Lys Glu Gly Glu Glu Asp	
205	965 970 975	
206	gga ttc tgg tgt att tgt gct gat gga ttt gaa gga gaa aat tgt gaa	2976
207	Gly Phe Trp Cys Ile Cys Ala Asp Gly Phe Glu Gly Glu Asn Cys Glu	
208	980 985 990	
209	gtc aac gtt gat gat tgt gaa gat aat gac tgt gaa aat aat tct aca	3024
210	Val Asn Val Asp Asp Cys Glu Asp Asn Asp Cys Glu Asn Asn Ser Thr	
211	995 1000 1005	
212	tgt gtc gat ggc att aat aac tac aca tgc ctt tgc cca cct gag tat	3072
213	Cys Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys Pro Pro Glu Tyr	
214	1010 1015 1020	
215	aca ggt gag ttg tgt gag gag aag ctg gac ttc tgt gcc cag gac ctg	3120
216	Thr Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys Ala Gln Asp Leu	
217	1025 1030 1035 1040	
218	aac ccc tgc cag cac gat tca aag tgc atc cta act cca aag gga ttc	3168
219	Asn Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr Pro Lys Gly Phe	
220	1045 1050 1055	
221	aaa tgt gac tgc aca cca ggg tac gta ggt gaa cac tgc gac atc gat	3216
222	Lys Cys Asp Cys Thr Pro Gly Tyr Val Gly Glu His Cys Asp Ile Asp	
223	1060 1065 1070	
224	ttt gac gac tgc caa gac aac aag tgt aaa aac gga gcc cac tgc aca	3264
225	Phe Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly Ala His Cys Thr	
226	1075 1080 1085	
227	gat gca gtg aac ggc tat acg tgc ata tgc ccc gaa ggt tac agt ggc	3312
228	Asp Ala Val Asn Gly Tyr Thr Cys Ile Cys Pro Glu Gly Tyr Ser Gly	
229	1090 1095 1100	
230	ttg ttc tgt gag ttt tct cca ccc atg gtc ctc cct cgt acc agc ccc	3360
231	Leu Phe Cys Glu Phe Ser Pro Pro Met Val Leu Pro Arg Thr Ser Pro	
232	1105 1110 1115 1120	
233	tgt gat aat ttt gat tgt cag aat gga gct cag tgt atc gtc aga ata	3408
234	Cys Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys Ile Val Arg Ile	
235	1125 1130 1135	
236	aat gag cca ata tgt cag tgt ttg cct ggc tat cag gga gaa aag tgt	3456
237	Asn Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Gln Gly Glu Lys Cys	
238	1140 1145 1150	
239	gaa aaa ttg gtt agt gtg aat ttt ata aac aaa gag tct tat ctt cag	3504
240	Glu Lys Leu Val Ser Val Asn Phe Ile Asn Lys Glu Ser Tyr Leu Gln	
241	1155 1160 1165	
242	att cct tca gcc aag gtt cgg cct cag acg aac ata aca ctt cag att	3552
243	Ile Pro Ser Ala Lys Val Arg Pro Gln Thr Asn Ile Thr Leu Gln Ile	
244	1170 1175 1180	

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION US/09/191,647DATE: 05/11/1999  
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Line	? Error/Warning	Original Text
572	W "N" or "Xaa" used: Feature required	Gln Phe Thr Asp Leu Gln Asn Trp Xaa Arg X
576	W "N" or "Xaa" used: Feature required	Asp His Ile Ala Val Xaa Leu Tyr Xaa Gly H
793	W "N" or "Xaa" used: Feature required	Arg Asn Pro Xaa Ile Cys Asp Cys Asn Leu G
807	W "N" or "Xaa" used: Feature required	Asp Leu Asn Ser Asn Ile His Val Leu Glu A
811	W "N" or "Xaa" used: Feature required	Leu Ser Lys Leu Arg Glu Leu Xaa Leu Asn A